

FIG.1

1 TGATCCTGTT CGAGAAGCTA CAAAATCAAA AGAAGGTGTA GAAATCATT
51 TCAACATTGA AGATGATAAT TCTGATAACG CATTGCAGTC CATGGAGAAG prat 119 ←
101 GATTTTCCA GACTGCGGAC ATCAAAATAA GCAAGAAGAT GATCAAAAAA
151 TGACAAAGCT AAGGAGTTTG AAGTAAGGCA AGGAACTTGA CACTGAATAT
201 CTAAGCTAAT TAGCAAGACT TTAGCAGCTT GTAATATTTA GTGTTTGTGA
251 GGTGTTACCT TATAATTAGC TTGTAGCATA GCCTTCCCAC TAATAATTCT prat 122 ←
301 GCTTAGCGAA TCTTATATAT GGGAAATACT TACACTAGTA TGCATCTTCT
351 ATATACATGT TTGGCACTTG ACTATACATA GAAAAATTAA CAAGCATTTT
401 TCACCTCAAT TTGTCACCTA CTTATAAGTA GCTGAATAAT ATAATGCAAT
451 TTTCAACCCC

FIG.2

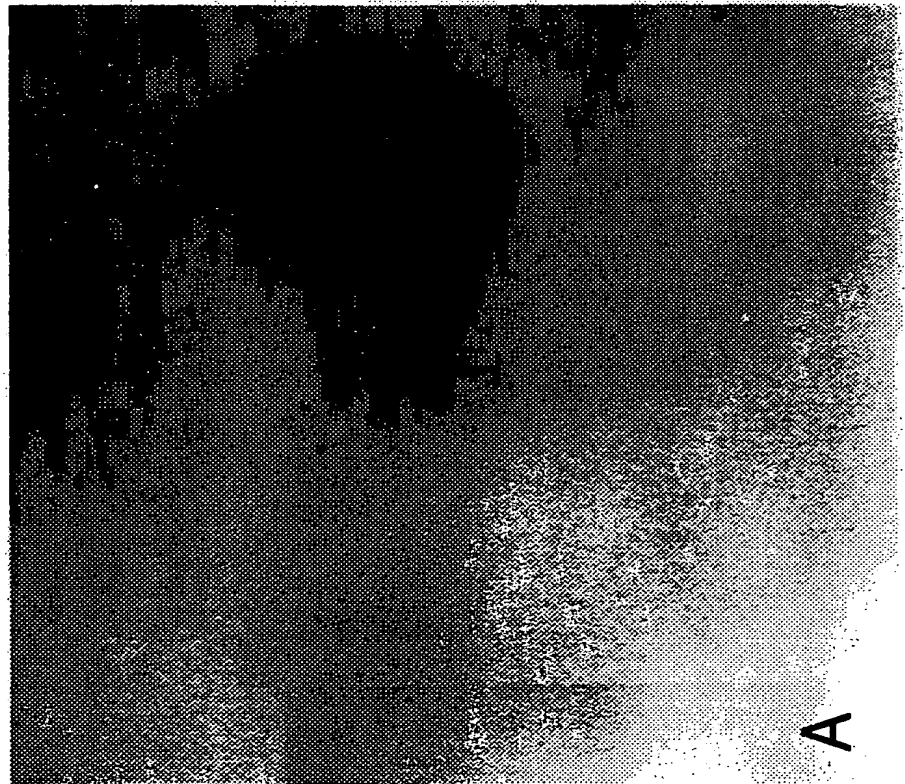
1 TCGAGCGGCC GCCCGGGCAG GTATTCAACA AGAGTATTCA CCACTTGAAC
51 TCAAAAGGGG CTTCACTAAA AAAAAATCAT GGCGCAATTA CGTGCTGATG prat 129 →
101 ACTTGTCTTT CATATTTGGC CTTCTTGGTA ATATTGTATC ATTCATGGTC
151 TTCCTAGCAC CCGTGCCAAC ATTTTACAAA ATATATAAAA GGAAATCATC
201 AGAAGGATAT CAAGCAATAC CATATATGGT AGCACTGTTC AGCGCCGGAC
251 TATTGCTATA TTATGCTTAT CTCAGGAAGA ATGCCTATCT TATCGTCAGC
301 ATTAATGGCT TTGGATGTGC CATTGAATTA ACATATATCT CTCTGTTTCT
351 CTTTTACGCG CCCAGAAAGT CTAAGATTTT CACAGGGTGG CTGATGCTCT
401 TAGAATTGGG AGCCCTAGGA ATGGTGATGC CAATTACTTA TTTATTAGCA
451 GAAGGCTCAC ATAGAGTGAT GATAGTGGGA TGGATTTGTG CAGCTATCAA
501 TGTTGCTGTC TTTGCTGCTC CTTTAAGCAT CATGAGGCAA GTAATAAAAA
551 CAAAGAGTGT AGAGTTCATG CCCTTCACTT TATCTTTGTT CCTCACTCTC
601 TGTGCCACTA TGTGGTTTTT CTATGGGTTT TTCAAGAAGG ACTTTTACAT
651 TGC GTTTCCA AATATACTGG GCTTTCTATT CGGAATCGTT CAAATGCTAT
701 TATATTTTGT TTACAAGGAT TCAAAGAGAA TAGATGATGA AAAATCTGAT
751 CCTGTTTCGAG AAGCTACAAA ATCAAAAGAA GGTGTAGAAA TCATTATCAA
801 CATTGAAGAT GATAATTCTG ATAACGCATT GCAGTCCATG GAGAAGG

FIG. 3

1 TCGAGCGGCC GCCCGGGCAG GTATTCAACA AGAGTATTCA CCACTTGAAC
51 TCAAAAGGGG CTTCACTAAA AAAAAATCAT GGC GCAATTA CGTGCTGATG
101 ACTTGCTCTT CATATTTGGC CTTCTTGGTA ATATTGTATC ATTCATGGTC
151 TTCCTAGCAC CCGTGCCAAC ATTTTACAAA ATATATAAAA GGAAATCATC
201 AGAAGGATAT CAAGCAATAC CATATATGGT AGCACTGTTC AGCGCCGGAC
251 TATTGCTATA TTATGCTTAT CTCAGGAAGA ATGCCTATCT TATCGTCAGC
301 ATTAATGGCT TTGGATGTGC CATTGAATTA ACATATATCT CTCTGTTTCT
351 CTTTTACGCG CCCAGAAAGT CTAAGATTTT CACAGGGTGG CTGATGCTCT
401 TAGAATTGGG AGCCCTAGGA ATGGTGATGC CAATTACTTA TTTATTAGCA
451 GAAGGCTCAC ATAGAGTGAT GATAGTGGGA TGGATTTGTG CAGCTATCAA
501 TGTGCTGTC TTTGCTGCTC CTTTAAGCAT CATGAGGCAA GTAATAAAAA
551 CAAAGAGTGT AGAGTTCATG CCCTTCACTT TATCTTTGTT CCTCACTCTC
601 TGTGCCACTA TGTGGTTTTT CTATGGGTTT TTCAAGAAGG ACTTTTACAT
651 TGC GTTTCCA AATATACTGG GCTTCTATT CGGAATCGTT CAAATGCTAT
701 TATATTTTGT TTACAAGGAT TCAAAGAGAA TAGATGATGA AAAATCTGAT
751 CCTGTTCGAG AAGCTACAAA ATCAAAAGAA GGTGTAGAAA TCATTATCAA
801 CATTGAAGAT GATAATTCTG ATAACGCATT GCAGTCCATG GAGAAGGATT
851 TTTCCAGACT GCGGACATCA AAATAAGCAA GAAGATGATC AAAAAATGAC
901 AAAGCTAAGG AGTTTGAAGT AAGGCAAGGA ACTTGACACT GAATATCTAA
951 GCTAATTAGC AAGACTTTAG CAGCTTGTA TATTTAGTGT TTGTGAGGTG
1001 TTACCTTATA ATTAGCTTGT AGCATAGCCT TCCCACTAAT AATTCTGCTT
1051 AGCGAATCTT ATATATGGGA AATACTTACA CTAGTATGCA TCTTCTATAT
1101 ACATGTTTGG CACTTGACTA TACATAGAAA AATTAACAAG CATTTCTCAC
1151 CTCAATTTGT CACTTACTTA TAAGTAGCTG AATAATATAA TGCAATTTTC
1201 ACCCC

FIG. 4

1 2 3 4 5 6



1 2 3 4 5 6

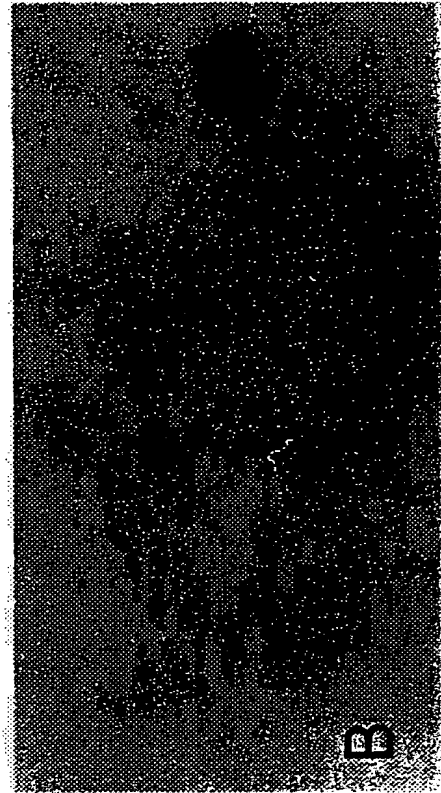


FIG.5

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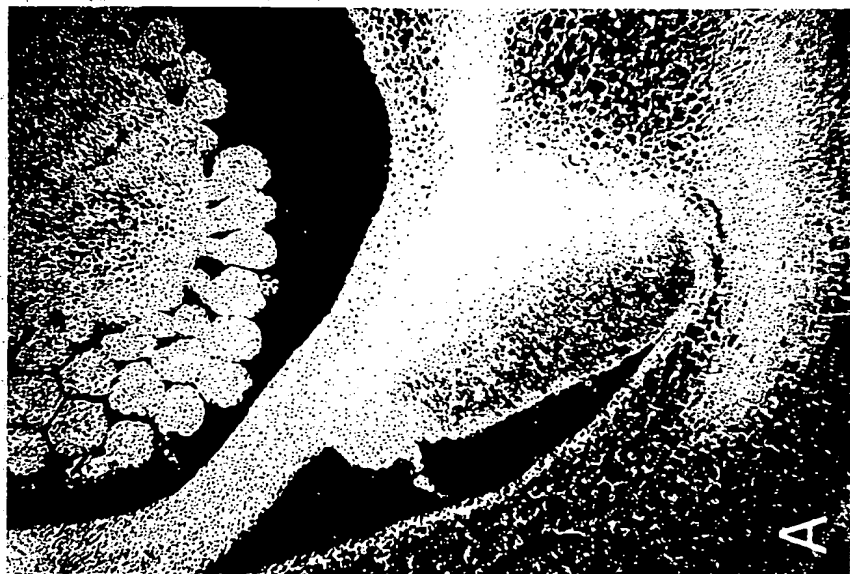
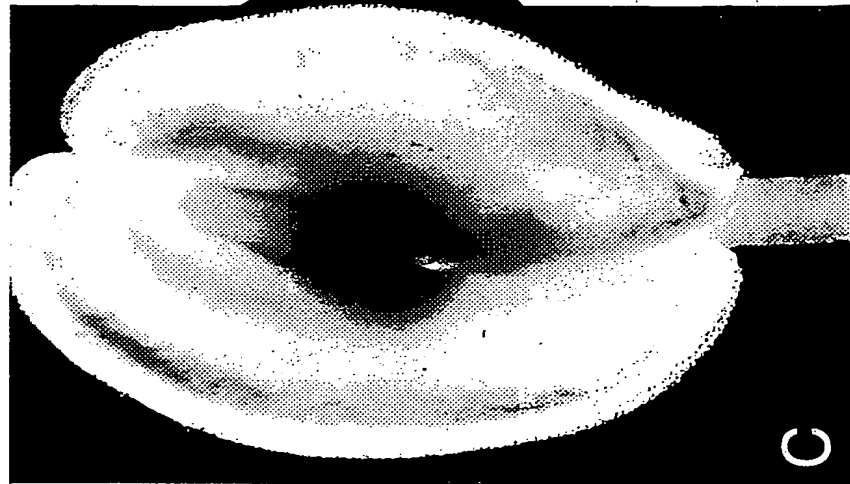


FIG. 6

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1 CCTAGGAGAAATCAAGCCTACTCTTAAGATGGATGACTCACTTGCCCCGA
51 TGGTAAGGTGAAGGATCTGTTGATTAGAGTTGGGAAGTTCATGTTCTCTG
101 CTGATTTTATTATTCTAGACTATGAAGAGGACCAAGAAGCTCCAATAATT
151 TTGGGAAGAGCATTCTTAATCACATCGATGGCAATTATTGACATGGAAC
201 TGGGGAGATGACTGTGAGAGCGCATGGAGAAAAGGTTACTTTCAAGGTTT
251 ATAATAAAAAGGATCATATGGCTAAGTTTGAAGAGTGTTCTTTGATAGAA
301 TGTGTCAGACGAGAACATGAAAGTAAACCGAAAGAGGTGTTTGAGCGGAA
351 TGTAGAACAAAGTGACCACGGCACAATAATTGACAAGTTGAAGGAAAATT
401 CACCTAAAGGAAGGAAGAAGACAAAAGTTCGTCGTAACAAGAGGAGACGT
451 AAATGCTGGAAGTGAGCTTAAAGGTGTTGTCTACTACGACGTTAACTAA
501 GCGCCTTGTCGGGAGGCAACCCTAGCTTTGTATGTAAATGTAAAAGTAA
551 AAATATATATATAGAAAAAGGAAAATACAAAAAGAGTCGTGCCGCGACGT
601 TAAATCAAGCGCTTGTTGGAAGGCAACCCAATTTTATTGTTTTAGTTGT
651 TTTACTTATTTAGTATTACGTAGTTTCTTGTTGTTTTTGTAGGGCTCGGG
701 ACTTTCGGAAGGTGAGGTAATTTCAAGGCATCGCGGTGTGTATTGCAGCG
751 AGGTAAGTGTAAGAGTTGAGTTGGAAGCGTTTGGCCAAGTGTTGCACCGT
801 GAGAGGCTTTCAACCTGTTGCGACACGTGAAAAATTAAGAGCCAGATCTG
851 CTACATTAGCACTGAAGCATCGCTTGGCCAATAGCTTGGAATGGAAGCAA
901 GAATTCAAACCAAAATCAGAAACGCCACAAGAGATGTGTGCGCACACTGCA
951 AAGCTTTGTGCAAACTAGTGAACGCAGAAATAGAAATGCTACAGCCCATG
1001 CGTCGCTTGGCTTATGGCAGGCAGCAAAAATTCAGCAGCAAAACAGAAAC
1051 GCTGCGAGAAACGCGTCGCATACGCCATAGCTTTGTGTCAAACAGAACGT
1101 CCAGAAATTGAAAAGCTATAAGCCTGCGTCGCTTGGCTCATGGCGTGCAG
1151 ACTAGAAAAGCTCTAGCAGATGCGTCGCGTATTGTATAGCTTGGTGTGAA
1201 ACAGAAAGTTCGAAACTTGGAAAACGATAACCCAGCGTCGCCTCTTCAAC
1251 CGCGTCCAGGTAAGTTCAAGATTCTTACGGGTGACCCATTAACCCATTG
1301 ATCGGCTGATTATAAACAATAAAACATCACCTTCAACTATCACATGATTT
1351 CATAAGTTTGACCTAGGATATTTTATATATATATATATATATATACACAC

FIG. 7

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1401 ACACACCATTTCCAGCGATCTTACCTCATTTTTATTCAAACCATTTTTCT
1451 GCTTCAAAAGTTTAAATTATTAATATGATAAGTCATCCATAGTCAAACAA
1501 GATTTTCTATACTATTTTGTCCCTTGTAATTTTAAAAAAAAAATGAGCGA
1551 TGGTAAGATAAACATTGTTTGCAAGTGTACAATTTTAGTATATGCAAACC
1601 AACGCTTCTTCTTCCAACATCACCTAAAACTACATCATTTATGGCGGGC
1651 GGACTAGACGTAGCCAAATATAAAAACGCAATGGCCATTTCAGTTCATGTC
1701 ATTTTTATATCCTTCATCCAATAATATTACTCAAATTTGATGTACAGTTT
1751 GGTCTCTGATGTGCACTTTACTATACGTAATACGGAATTTACATTATAAT
1801 TAAAGAGAACTGTTCCACTAAATTTTAATGATTTAATTAATTTAACTCGG
1851 TTACTTGTATTATTATTATTGCTGTATTTGTTTGTCAATTTGAATTTGGCA
1901 CCGCAGATTTTGTATGCAATTAACCTCATATATCTTTTGGCCAAATAA
1951 AGAAAAAGTCTGCATATTTCTTGCCAAACATTTATCATACTTTACCGAAT
2001 TCTTGTTTTTTGTTTCTCTGTTGTTGTTCTCCACTATAAATAACATTTGC
2051 AGTGAGTAAAGTTTCTTCAGGTCTCTTTTGTAGATTCAACAAGAGTATTC
2101 AGCACTTGAACCTCAAAGGGGCTTCACTAAAAAAAATCATG

FIG.7(CONTIN.)

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PBNEP1

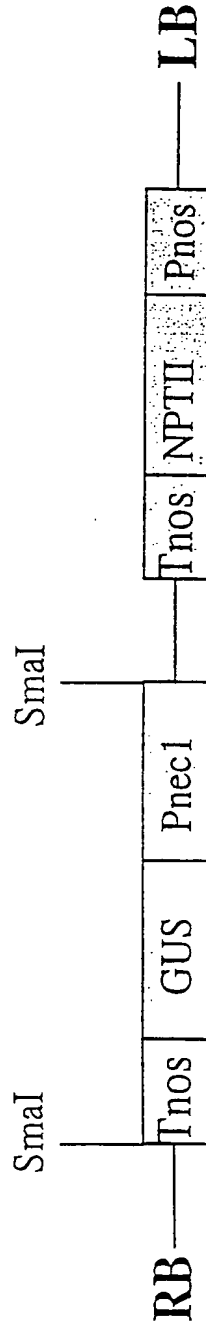


FIG. 8

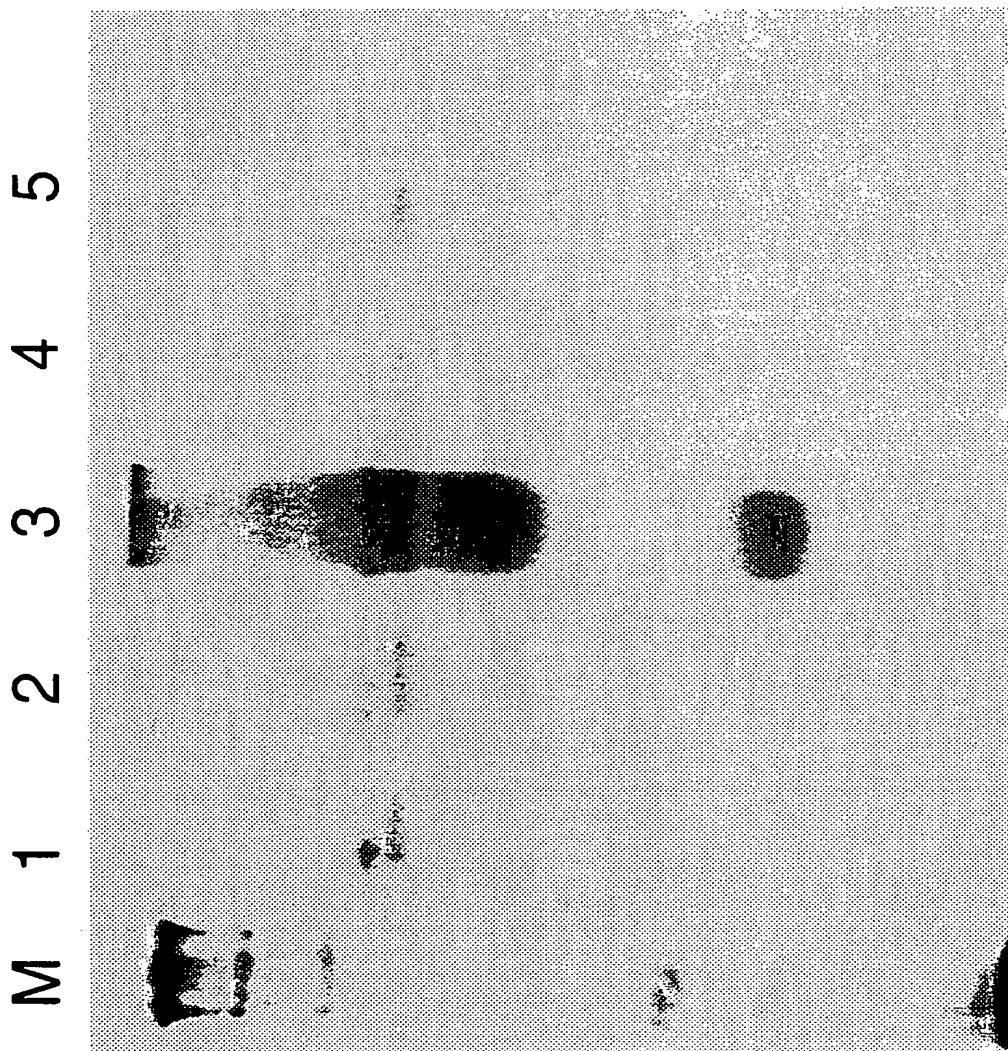


FIG. 9

SDS page of honey and nectar

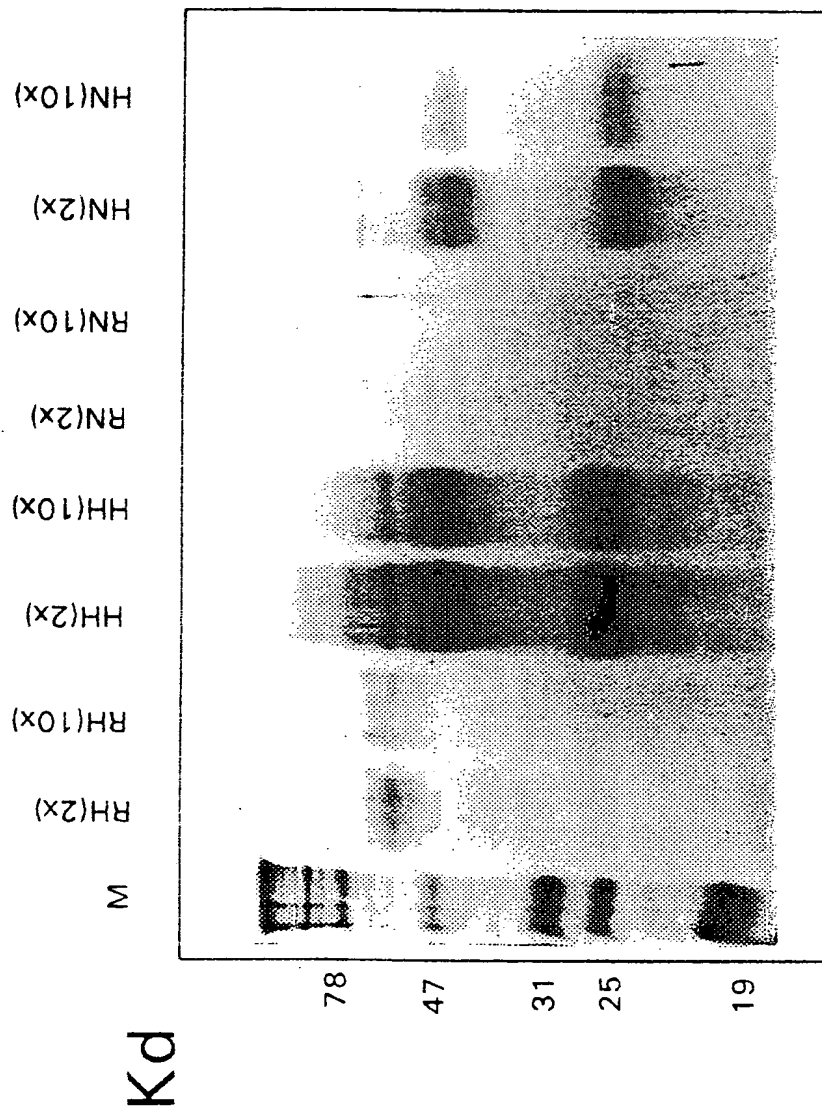


FIG.10

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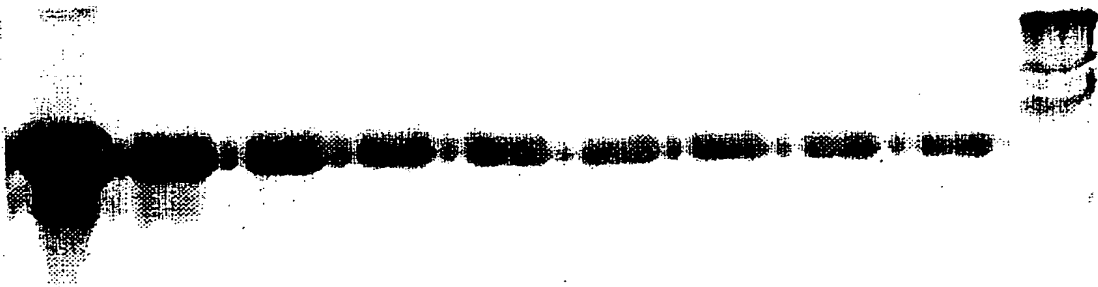
PCT/NL99/00453

1 2 3 4 5 6 7 8 9



A

1 2 3 4 5 6 7 8 9 M



B

FIG. 11

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===17-APR-1998=====PC/GENE===

 * ALIGNMENT OF TWO PROTEIN SEQUENCES. *

The two sequences to be aligned are:

PCVH29.

Total number of residues: 60.

GER1.

Total number of residues: 211.

Comparison matrix : Structure-genetic matrix.

Open gap cost : 7

Unit gap cost : 1

The character to show that two aligned residues are identical is '|'

```
PCVH29 - MKMFLPILFTISLLFSSSHASVLD FCVADPSLPDGPAGYSCKEPAKVTVD -50
      ||| | | | | | | | | | | | | | | | | | | | | | | | | |
GER1    - MKMRIQIFFILSLFSSISFASVQDFCVADPKGPQNPSGYCKNPDQVTEN -50

PCVH29 - DFVFHGLGTA -60
      || | | | | |
GER1    - DFAFSGLGKAGNTSNVIKAAVTPAFAPAFAGLNGLDVSLARLDLAGGGVI -100

GER1    - PLHTHPGASEVLVVIQGTICAGFISSANKVYLKTL SRGDSMVFPQGLLHF -150

GER1    - QLNSGKGPALAFVAFGSSSPGLQILPFALFANDLPSELVEATTFLSDEEV -200

GER1    - KKLKGVLGGTN -211
```

Identity : 36 (60%)

Number of gaps inserted in PCVH29: 0

Number of gaps inserted in GER1: 0

===17-APR-1998=====PC/GENE===

FIG.12

Ser - Val - Leu - Asp - Phe - Cys - Val - Ala - Asp - Pro - Ser - Leu - Pro
 TCA GT* CT* GAC TTC TGC GT* GC* GAC CC* TC* CT* CC*
 TCC TTA GAT TTT TGT GAT AGC TTA
 TCG TTG
 TCT
 AGC
 AGT

→ prat 176

Asp - Gly - Pro - Ala - Gly - Tyr - Ser - Cys - Lys - Glu - Pro - Ala - Lys - Val
 GAC GG* CC* GC* GG* TAC TC* TGC AAA GAA CC* GC* TGC GT*
 TAT AGC TGT AAG GAG
 AGT

Thr - Val - Asp - Asp - Phe - Val - Phe - His - Gly - Leu - Gly - Thr - Ala
 AC* GT* GAC GAC TTC GT* TTC CAC GG* CT* GG* AC* GC*
 GAT GAT TTT TTT CAT TTA TTG

← prat 177

Ser - Val - Leu - Asp - Phe - Cys - Val - Ala - Asp - Pro - Ser - Leu - Pro
 TCA GT* CT* GAT TTC TGT GTG GCT GAT CCA TCC TTG CCC
 TCC TTA
 TCG TTG
 TCT
 AGC
 AGT

Asp - Gly - Pro - Ala - Gly - Tyr - Ser - Cys - Lys - Glu - Pro - Ser - Lys - Val
 GAT GGC CCT GCA GGC TAC TCC TGC AAG GAG CCC TCT AAA GTC

Thr - Val - Asp - Phe - Val - Phe - His - Gly - Leu - Gly - Thr - Ala
 ACC GTA GAC GAT TTC GT* TTC CAC GG* CT* GG* AC* GC*
 TTA TTG

→

prat 206 ← prat 204
 prat 207 ← prat 205

A

B

FIG.13

MAR5H6 CGCCCGGGCTGGTAAACAAAGTACGCTGTATATACTCATTTGTATTTCCTTAAA 50
MAR5R8 CGCCCGGGCTGGTAAACAAAGTACGCTGTATATACTCATTTGTATTTCCTTAAA 50
MAR5R6 GGCCCGGGCTGGTAAACAAAGTACGCTGTATATACTCATTTGTATTTCCTTAAA 50
MAR5H8 CGCCCGGGCTGGTAAACAAAGTACGCTGTATATACTCATTTGTATTTCCTTAAA 50

MAR5H6 AAAGCAACTGTCAAAAATTCGACCAAAACGAGTATATAAGTATCACTTTCC 100
MAR5R8 AAAGCAACTGTCAAAAATTCGACCAAAACGAGTATATAAGTATCACTTTCC 100
MAR5R6 AAAGCAACTGTCAAAAATTCGACCAAAACGAGTATATAAGTATCACTTTCC 100
MAR5H8 AA - GCAACTGTCAAAAATTCGACCAAAACGAGTATATAAGTATCACTTTCC 99
** *****
MAR5H6 CCCTATTGGACAACACGAACTCTAAGAGGGCAATCAGACACACCCAGCCAT 150
MAR5R8 CCCTATTGGACAACACGAACTCTAAGAGGGCAATCAGACACACCCAGCCAT 150
MAR5R6 CCCTATTGGACAACACGAACTCTAAGAGGGCAATCAGACACACCCAGCCAT 150
MAR5H8 CCCTATTAAACACCCAGAACTCTAAGAGGGCAATCAGACACACCCAGCCAT 149

MAR5H6 TGCACCTTGTAAGATGTTTCTTCCAAATCTCTTCCACCATTTCCCTCCTCT 200
MAR5R8 TGCACCTTGTAAGATGTTTCTTCCAAATCTCTTCCACCATTTCCCTCCTCT 200
MAR5R6 TGCACCTTGTAAGATGTTTCTTCCAAATCTCTTCCACCATTTCCCTCCTCT 200
MAR5H8 TGCACCTTATGAAGATGTTTCTTCCAAATCTCTTCCACCATTTCCCTCCTCT 199

signal sequence ← mature protein
MAR5H6 TCTCCTCTCCCATGCTTCAGTGTGGACTTCTGCGTAGCAGACCCATCC 250
MAR5R8 TCTCCTCTCCCATGCTTCAGTGTGGACTTCTGCGTAGCAGACCCATCC 250
MAR5R6 TCTCCTCTCCCATGCTTCAGTGTGGACTTCTGCGTAGCAGACCCATCC 250
MAR5H8 TCTCCTCTCCCATGCTTCAGTGTGGACTTCTGCGTAGCAGACCCATCC 249

FIG. 14

tatgttccttccaattcttttcactatctctctctctctctctctctcatgcttctgttcttgatttcg
acaagggaagggttaagaaaaagtataaagagaagaaaaagagaagagagtagcgaagacaagaactaaagcctag

FIG.15

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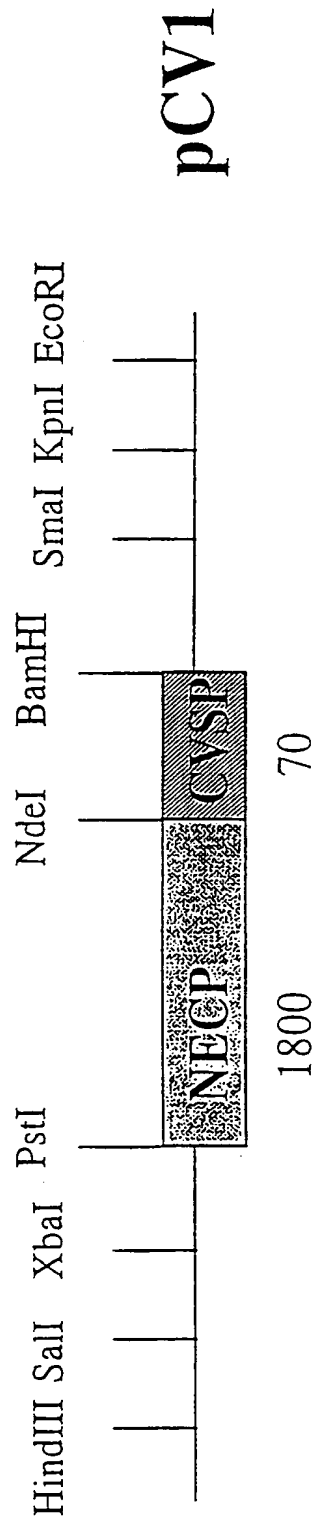


FIG.16

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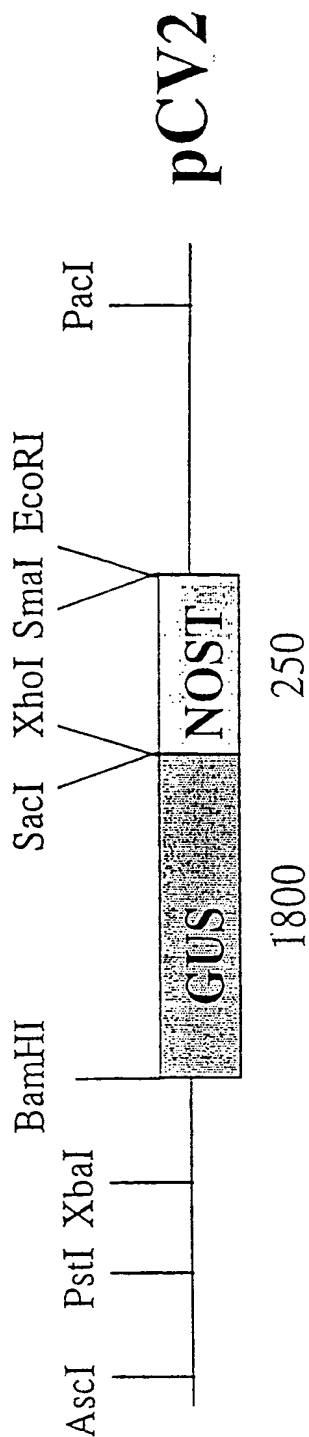


FIG.17

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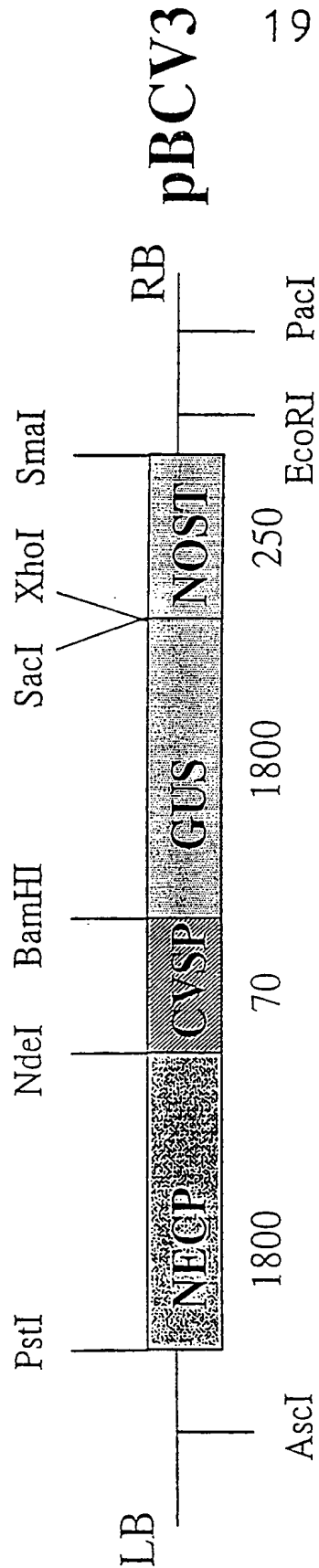


FIG. 18

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1 TCTGAATACAAGCTGTGTGTAGAGAGATTTCTATAAAGACAGCAAACAT
51 CCCTTCTTTTTGTTCTGTTTTTAAAAGTCCCTTCTTCAACCAGCTCTTTT
101 CCTCATCAGGGTAAGTTGCAAATAAAGGGGATGTTCCAGAATCAAGAAGA
151 GAAGATGTCAGACTCGCCTCAGAGGAAGATGGAAGAGGAAAGATTGAGA
201 TTAAGAGGATTGAAAATACAACAAATCGTCAAGTCACTTTCTGTAAGAGA
251 AGAAATGGGTTGCTTAAAAAAGCTTATGAACCTTCTGTTCTTTGTGATGC
301 TGAAGTTGCTCTCATCGTTTTCTCAAGCCGTGGCCGCTCTATGAATATG
351 CTAACAACAGTGTGAAGGCAACAATTGATAGATATAAGAAAGCATCCTCA
401 GATTCTCCAACACTGGATCTACTTCTGAAGCTAACACTCAGTTTTATCA
451 ACAAGAAGCTGCCAAACTCCGAGTTCAGATTGGTAACTTACAGAACTCAA
501 ACAGGAACATGCTAGGCGAGTCTCTAAGTTCTCTGACTGCAAAAGATCTG
551 AAAGGCCTGGAGACCAAACTTGAGAAAGGAATTAGTAGAATTAGGTCCAA
601 AAAGAATGAACTCCTGTTTGCTGAGATTGAGTATATGCGAAAAAGGGAAA
651 TTGATTTGCACAACAACAATCAGATGCTTCGGGCAAAGATAGCTGAGAGT
701 GAAAGAAATGTGAACATGATGGGAGGAGAATTTGAGCTGATGCAATCTCA
751 TCCGTACGATCCAAGAGACTTCTTCCAAGTGAACGGCTTACAGCATAATC
801 ATCAATATCCACGCCAAGACAACATGGCTCTTCAATTAGTATAGTTTAT
851 AATAAAATGCATGGTTTGAAGCACTCTGATTGTGGTGGATTGGATTATG
901 TATAAGGGAGTGCAGGCCATTTGCCAATTATTGAAAGGTACTCAAACAGG
951 AAGTTGAAGAAGTTCATCATCTCTCATCTATATGTCTTAACAAAAGTC
1001 TTAGCTTATGGACTCTAAAACAAAGACTTAATTTAACATATAAATATAAT
1051 TGTGTAATGCTGTTGTATTGTATGGTATGTATCCAAAAACATTAATAACC
1101 TATCTTTTCTTCAAATTATGTCTCCTTTGATACAACTACTAACATATT
1151 TTCTTAT

MADS-box

K-box

FIG.19